SEQUENCE LISTING

<110> Kadler, Karl
        Bulleid, Neil
        Ashcroft, Gillian

<120> Modified Peptides and Their Uses

<130> 17695-0002

<140> US 10/554,068
<141> 2005-10-21

<150> PCT/GB2004/00171
<151> 2004-04-21

<150> GB 0309064.4
<151> 2003-04-22

<160> 28

<170> PatentIn version 3.3

<210> 1
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<212> DNA
<213> Artificial Sequence

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<223> Oligonucleotide for PCR

<400> 1
aattaccct cactaaaggg   20

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acagagatgt tgccaaaata atagtgggat g   31

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tattttggca acatctctgt ccttgtttct c   31

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cttgaccatt agcatcttgc cacaccttca c                              31


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gttgtaaaac ggcggccgct gaattgtaat ac                             32


<210>  8
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<400> 8
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<211> 5853
<212> DNA
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<220>
<223> DNA molecule based on procollagen type III N-propeptide.
      Sequence prior to N100 replaced with the sequence for the G123
      domains of the alpha3 chain of laminin-5 whilst retaining the
      collagen III signal sequence.

<400> 9
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actgagaata tgtttgtgat gtaccttgga aataaagatg cctcccggga ctacatcggc   180

atggcagttg tggatggcca gctcacctgt gtctacaacc tgggggaccg tgaggctgaa   240

ctccaagtgg accagatctt gaccaagagt gagactaagg aggcagttat ggatcgggtg   300

aaatttcaga gaatttatca gtttgcaagg cttaattaca ccaaaggagc cacatccagt   360

aaaccagaaa cacccggagt ctatgacatg gatggtagaa atagcaatac actccttaat   420

ttggatcctg aaaatgttgt attttatgtt ggaggttacc cacctgattt taaacttccc   480

agtcgactaa gtttccctcc atacaaaggt tgtattgaat tagatgacct caatgaaaat   540

gttctgagct tgtacaactt caaaaaaaca ttcaatctca cacaactga agtggagcct   600

tgtagaagga ggaaggaaga gtcagacaaa aattattttg aaggtacggg ctatgctcga   660

gttccaactc aaccacatgc tcccatccca acctttggac agacaattca gaccaccgtg   720

gatagaggct gctgttctt tgcagaaaac ggggatcgct tcatatctct aaatatagaa   780

gatggcaagc tcatggtgag atacaaactg aattcagagc taccaaaaga gagaggagtt   840

ggagacgcca taaacaacgg cagagaccat tcgattcaga tcaaaattgg aaaactccaa   900

aagcgtatgt ggataaatgt ggacgttcaa aacactataa ttgatggtga agtatttgat   960

ttcagcacat attatctggg aggaattcca attgcaatca gggaaagatt taacatttct   1020

acgcctgctt tccgaggctg catgaaaaat ttgaagaaaa ccagtggtgt cgttagattg   1080

aatgatactg tgggagtaac caaaaagtgc tcggaagact ggaagcttgt gcgatctgcc   1140

tcattctcca gaggaggaca attgagtttc actgatttgg cttaccacc tactgaccac   1200

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gatagcggcg gcccaatttt taaatctcca cagacgtata·tggatggttt actgcattat      1380

gtatctgtaa taagcgacaa ctctggacta cggcttctca tcgatgacca gcttctgaga      1440

aatagcaaaa ggctaaaaca catttcaagt tcccggcagt ctctgcgtct gggcgggagc      1500

aattttgagg gttgtattag caatgttttt gtccagaggt tatcactgag tcctgaagtc      1560

ctagatttga ccagtaactc tctcaagaga gatgtgtccc tgggaggctg cagtttaaac      1620

aaaccacctt ttctaatgtt gcttaaaggt tctaccaggt ttaacaagac caagactttt      1680

cgtatcaacc agctgttgca ggacacacca gtggcctccc caaggagcgt gaaggtgtgg      1740

caagatgcta atggtcaagg acctcaaggc cccaagggag atccaggccc tcctggtatt      1800

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ccccctggaa tctgtgaatc atgccctact ggtcctcaga actattctcc ccagtatgat      1920

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ggccccccag gccctcccgg tccccctggt acatctggtc atcctggttc ccctggatct      2040

ccaggatacc aaggaccccc tggtgaacct gggcaagctg gtccttcagg ccctccagga      2100

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cctggattcc ctggtatgaa aggacacaga ggcttcgatg gacgaaatgg agaaaagggt      2280

gaaacaggtg ctcctggatt aaagggtgaa aatggtcttc caggcgaaaa tggagctcct      2340

ggacccatgg gtccaagagg ggctcctggt gagcgaggac ggccaggact tcctgggget      2400

gcaggtgctc ggggtaatga cggtgctcga ggcagtgatg gtcaaccagg ccctcctggt      2460

cctcctggaa ctgccggatt ccctggatcc cctggtgcta agggtgaagt tggacctgca      2520

gggtctcctg gttcaaatgg tgcccctgga caaagaggag aacctggacc tcaggacac      2580

gctggtgctc aaggtcctcc tggccctcct gggattaatg gtagtcctgg tggtaaaggc      2640

gaaatgggtc ccgctggcat tcctggagct cctggactga tgggagcccg gggtcctcca      2700

ggaccagccg gtgctaatgg tgctcctgga ctgcgaggtg gtgcaggtga gcctggtaag      2760

aatggtgcca aaggagagcc cggaccacgt ggtgaacgcg gtgaggctgg tattccaggt      2820

gttccaggag ctaaaggcga agatggcaag gatggatcac ctggagaacc tggtgcaaat      2880

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aatggcatcc caggagaaaa gggtcctgct ggagagcgtg gtgctccagg ccctgcaggg      3000

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ggcatgcccg gaagtccagg aggaccagga agtgatggga aaccagggcc tcccggaagt      3120

caaggagaaa gtggtcgacc aggtcctcct gggccatctg gtccccgagg tcagcctggt      3180

gtcatgggct tccccggtcc taaaggaaat gatggtgctc ctggtaagaa tggagaacga      3240

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ggggaaccag gtccaaaggg tgatgccggt gcacctggag ctccaggagg caagggtgat      3480

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ggtgctgctg gtactcctgg tctgcaagga atgcctggag aaagaggagg tcttggaagt      3660

cctggtccaa agggtgacaa gggtgaacca ggcggcccag gtgctgatgg tgtcccaggg      3720

aaagatggcc aaggggtcc tactggtcct attggtcctc ctggcccagc tggccagcct      3780

ggagataagg gtgaaggtgg tgcccccgga cttccaggta tagctggacc tcgtggtagc      3840

cctggtgaga gaggtgaaac tggccctcca ggacctgctg gtttccctgg tgctcctgga      3900

cagaatggtg aacctggtgg taaaggagaa agaggggctc cgggtgagaa aggtgaagga      3960

ggccctcctg gagttgcagg accccctgga ggttctggac ctgctggtcc tcctggtccc      4020

caaggtgtca aaggtgaacg tggcagtcct ggtggacctg gtgctgctgg cttccctggt      4080

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ggatcagatg gtcttccagg ccgagatgga tctcctggtg gcaagggtga tcgtggtgaa      4560

aatggctctc ctggtgcccc tggcgctcct ggtcatccag gcccacctgg tcctgtcggt      4620
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gccccaggtt ctccaggccc tgctggtcag cagggtgcaa tcggcagtcc aggacctgca    4860

ggccccagag gacctgttgg acccagtgga cctcctggca aagatggaac cagtggacat    4920

ccaggtccca ttggaccacc agggcctcga ggtaacagag gtgaaagagg atctgagggc    4980

tccccaggcc acccagggca accaggccct cctggacctc ctggtgcccc tggtccttgc    5040

tgtggtggtg ttggagccgc tgccattgct gggattggag gtgaaaaagc tggcggtttt    5100

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cagtttagct acggcaatcc tgaacttcct gaagatgtcc ttgatgtgca gctggcattc    5520

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<213>   Artificial Sequence

<220>
<223>   Sequence of the modified pro-alpha chain

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1               5                   10                  15
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His Pro Thr Ile Ile Leu Ala Thr Ser Leu Ser Leu Phe Leu Gln Arg
        20   25   30

Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr
        35   40   45

Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val
    50   55   60

Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu
65   70   75   80

Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val
            85   90   95

Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn
            100   105   110

Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr
        115   120   125

Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu
    130   135   140

Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro
145   150   155   160

Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp
            165   170   175

Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn
            180   185   190

Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser
        195   200   205

Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln
    210   215   220

Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val
225   230   235   240

Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser

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Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser
        260   265   270

Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg
        275   280   285

Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp
    290   295   300

Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp
305   310   315   320

Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg
            325   330   335

Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys
            340   345   350

Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys
        355   360   365

Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg
        370   375   380

Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr Asp His
385   390   395   400

Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Ile Leu
            405   410   415

Leu Asp His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu Glu Asp
            420   425   430

Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys
        435   440   445

Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile
    450   455   460

Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg
465   470   475   480

```
Asn Ser Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg
            485                 490                 495

Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln
            500                 505                 510

Arg Leu Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu
            515                 520                 525

Lys Arg Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe
    530             535             540

Leu Met Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys Thr Phe
545             550                 555                 560

Arg Ile Asn Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro Arg Ser
            565                 570             575

Val Lys Val Trp Gln Asp Ala Asn Gly Gln Gly Pro Gln Gly Pro Lys
            580             585                 590

Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly
            595             600             605

Ile Pro Gly Gln Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile
    610             615             620

Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp
625             630             635                 640

Ser Tyr Asp Val Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr
            645             650             655

Pro Gly Pro Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Ser
            660             665             670

Gly His Pro Gly Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly
            675             680             685

Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Ala
    690             695             700
```

Ile Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro
705   710   715   720

Gly Arg Pro Gly Glu Arg Gly Leu Pro Gly Pro Gly Ile Lys Gly
            725   730   735

Pro Ala Gly Ile Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe
                740   745   750

Asp Gly Arg Asn Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys
            755   760   765

Gly Glu Asn Gly Leu Pro Gly Glu Asn Gly Ala Pro Gly Pro Met Gly
        770   775   780

Pro Arg Gly Ala Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala
785   790   795   800

Ala Gly Ala Arg Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro
                805   810   815

Gly Pro Pro Gly Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser Pro Gly
            820   825   830

Ala Lys Gly Glu Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala
        835   840   845

Pro Gly Gln Arg Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln
    850   855   860

Gly Pro Pro Gly Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly
865   870   875   880

Glu Met Gly Pro Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala
                885   890   895

Arg Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly Ala Pro Gly Leu Arg
            900   905   910

Gly Gly Ala Gly Glu Pro Gly Lys Asn Gly Ala Lys Gly Glu Pro Gly
        915   920   925

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```
Pro Arg Gly Glu Arg Gly Glu Ala Gly Ile Pro Gly Val Pro Gly Ala
   930             935             940

Lys Gly Glu Asp Gly Lys Asp Gly Ser Pro Gly Glu Pro Gly Ala Asn
945             950             955             960

Gly Leu Pro Gly Ala Ala Gly Glu Arg Gly Ala Pro Gly Phe Arg Gly
         965             970             975

Pro Ala Gly Pro Asn Gly Ile Pro Gly Glu Lys Gly Pro Ala Gly Glu
         980             985             990

Arg Gly Ala Pro Gly Pro Ala Gly  Pro Arg Gly Ala Ala  Gly Glu Pro
         995             1000             1005

Gly Arg  Asp Gly Val Pro Gly  Gly Pro Gly Met Arg  Gly Met Pro
   1010             1015             1020

Gly Ser  Pro Gly Gly Pro Gly  Ser Asp Gly Lys Pro  Gly Pro Pro
   1025             1030             1035

Gly Ser  Gln Gly Glu Ser Gly  Arg Pro Gly Pro Pro  Gly Pro Ser
   1040             1045             1050

Gly Pro  Arg Gly Gln Pro Gly  Val Met Gly Phe Pro  Gly Pro Lys
   1055             1060             1065

Gly Asn  Asp Gly Ala Pro Gly  Lys Asn Gly Glu Arg  Gly Gly Pro
   1070             1075             1080

Gly Gly  Pro Gly Pro Gln Gly  Pro Pro Gly Lys Asn  Gly Glu Thr
   1085             1090             1095

Gly Pro  Gln Gly Pro Pro Gly  Pro Thr Gly Pro Gly  Gly Asp Lys
   1100             1105             1110

Gly Asp  Thr Gly Pro Pro Gly  Pro Gln Gly Leu Gln  Gly Leu Pro
   1115             1120             1125

Gly Thr  Gly Gly Pro Pro Gly  Glu Asn Gly Lys Pro  Gly Glu Pro
   1130             1135             1140

Gly Pro  Lys Gly Asp Ala Gly  Ala Pro Gly Ala Pro  Gly Gly Lys
```

```
        1145                    1150                    1155

   Gly Asp  Ala Gly Ala Pro Gly  Glu Arg Gly Pro Pro  Gly Leu Ala
        1160                    1165                    1170

   Gly Ala  Pro Gly Leu Arg Gly  Gly Ala Gly Pro Pro  Gly Pro Glu
        1175                    1180                    1185

   Gly Gly  Lys Gly Ala Ala Gly  Pro Pro Gly Pro Pro  Gly Ala Ala
        1190                    1195                    1200

   Gly Thr  Pro Gly Leu Gln Gly  Met Pro Gly Glu Arg  Gly Gly Leu
        1205                    1210                    1215

   Gly Ser  Pro Gly Pro Lys Gly  Asp Lys Gly Glu Pro  Gly Gly Pro
        1220                    1225                    1230

   Gly Ala  Asp Gly Val Pro Gly  Lys Asp Gly Pro Arg  Gly Pro Thr
        1235                    1240                    1245

   Gly Pro  Ile Gly Pro Pro Gly  Pro Ala Gly Gln Pro  Gly Asp Lys
        1250                    1255                    1260

   Gly Glu  Gly Gly Ala Pro Gly  Leu Pro Gly Ile Ala  Gly Pro Arg
        1265                    1270                    1275

   Gly Ser  Pro Gly Glu Arg Gly  Glu Thr Gly Pro Pro  Gly Pro Ala
        1280                    1285                    1290

   Gly Phe  Pro Gly Ala Pro Gly  Gln Asn Gly Glu Pro  Gly Gly Lys
        1295                    1300                    1305

   Gly Glu  Arg Gly Ala Pro Gly  Glu Lys Gly Glu Gly  Gly Pro Pro
        1310                    1315                    1320

   Gly Val  Ala Gly Pro Pro Gly  Gly Ser Gly Pro Ala  Gly Pro Pro
        1325                    1330                    1335

   Gly Pro  Gln Gly Val Lys Gly  Glu Arg Gly Ser Pro  Gly Gly Pro
        1340                    1345                    1350

   Gly Ala  Ala Gly Phe Pro Gly  Ala Arg Gly Leu Pro  Gly Pro Pro
        1355                    1360                    1365
```

```
Gly Ser   Asn Gly Asn Pro Gly   Pro Pro Gly Pro Ser   Gly Ser Pro
    1370                1375                  1380

Gly Lys   Asp Gly Pro Pro Gly   Pro Ala Gly Asn Thr   Gly Ala Pro
    1385                1390                  1395

Gly Ser   Pro Gly Val Ser Gly   Pro Lys Gly Asp Ala   Gly Gln Pro
    1400                1405                  1410

Gly Glu   Lys Gly Ser Pro Gly   Ala Gln Gly Pro Pro   Gly Ala Pro
    1415                1420                  1425

Gly Pro   Leu Gly Ile Ala Gly   Ile Thr Gly Ala Arg   Gly Leu Ala
    1430                1435                  1440

Gly Pro   Pro Gly Met Pro Gly   Pro Arg Gly Ser Pro   Gly Pro Gln
    1445                1450                  1455

Gly Val   Lys Gly Glu Ser Gly   Lys Pro Gly Ala Asn   Gly Leu Ser
    1460                1465                  1470

Gly Glu   Arg Gly Pro Pro Gly   Pro Gln Gly Leu Pro   Gly Leu Ala
    1475                1480                  1485

Gly Thr   Ala Gly Glu Pro Gly   Arg Asp Gly Asn Pro   Gly Ser Asp
    1490                1495                  1500

Gly Leu   Pro Gly Arg Asp Gly   Ser Pro Gly Gly Lys   Gly Asp Arg
    1505                1510                  1515

Gly Glu   Asn Gly Ser Pro Gly   Ala Pro Gly Ala Pro   Gly His Pro
    1520                1525                  1530

Gly Pro   Pro Gly Pro Val Gly   Pro Ala Gly Lys Ser   Gly Asp Arg
    1535                1540                  1545

Gly Glu   Ser Gly Pro Ala Gly   Pro Ala Gly Ala Pro   Gly Pro Ala
    1550                1555                  1560

Gly Ser   Arg Gly Ala Pro Gly   Pro Gln Gly Pro Arg   Gly Asp Lys
    1565                1570                  1575
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Gly Glu   Thr Gly Glu Arg Gly   Ala Ala Gly Ile Lys   Gly His Arg
    1580                1585                    1590


Gly Phe   Pro Gly Asn Pro Gly   Ala Pro Gly Ser Pro   Gly Pro Ala
    1595                1600                    1605


Gly Gln   Gln Gly Ala Ile Gly   Ser Pro Gly Pro Ala   Gly Pro Arg
    1610                1615                    1620


Gly Pro   Val Gly Pro Ser Gly   Pro Pro Gly Lys Asp   Gly Thr Ser
    1625                1630                    1635


Gly His   Pro Gly Pro Ile Gly   Pro Pro Gly Pro Arg   Gly Asn Arg
    1640                1645                    1650


Gly Glu   Arg Gly Ser Glu Gly   Ser Pro Gly His Pro   Gly Gln Pro
    1655                1660                    1665


Gly Pro   Pro Gly Pro Pro Gly   Ala Pro Gly Pro Cys   Cys Gly Gly
    1670                1675                    1680


Val Gly   Ala Ala Ala Ile Ala   Gly Ile Gly Gly Glu   Lys Ala Gly
    1685                1690                    1695


Gly Phe   Ala Pro Tyr Tyr Gly   Asp Glu Pro Met Asp   Phe Lys Ile
    1700                1705                    1710


Asn Thr   Asp Glu Ile Met Thr   Ser Leu Lys Ser Val   Asn Gly Gln
    1715                1720                    1725


Ile Glu   Ser Leu Ile Ser Pro   Asp Gly Ser Arg Lys   Asn Pro Ala
    1730                1735                    1740


Arg Asn   Cys Arg Asp Leu Lys   Phe Cys His Pro Glu   Leu Lys Ser
    1745                1750                    1755


Gly Glu   Tyr Trp Val Asp Pro   Asn Gln Gly Cys Lys   Leu Asp Ala
    1760                1765                    1770


Ile Lys   Val Phe Cys Asn Met   Glu Thr Gly Glu Thr   Cys Ile Ser
    1775                1780                    1785
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Ala Asn Pro Leu Asn Val Pro Arg Lys His Trp Trp Thr Asp Ser
    1790   1795   1800

Ser Ala Glu Lys Lys His Val Trp Phe Gly Glu Ser Met Asp Gly
    1805   1810   1815

Gly Phe Gln Phe Ser Tyr Gly Asn Pro Glu Leu Pro Glu Asp Val
    1820   1825   1830

Leu Asp Val Gln Leu Ala Phe Leu Arg Leu Leu Ser Ser Arg Ala
    1835   1840   1845

Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met
    1850   1855   1860

Asp Gln Ala Ser Gly Asn Val Lys Lys Ala Leu Lys Leu Met Gly
    1865   1870   1875

Ser Asn Glu Gly Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe Thr
    1880   1885   1890

Tyr Thr Val Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp
    1895   1900   1905

Ser Lys Thr Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu
    1910   1915   1920

Pro Ile Val Asp Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln
    1925   1930   1935

Glu Phe Gly Val Asp Val Gly Pro Val Cys Phe Leu
    1940   1945   1950

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for PCR

<400> 11
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<210> 12

<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for PCR

<400> 12
cccactatta ttttggcatg ctcggaagac tggaagc   37

<210> 13
<211> 4815
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA molecule based on procollagen type III N-propeptide.
      Sequence prior to N100 replaced with the sequence for the G3
      domain of the alpha3 chain of laminin-5 whilst retaining the
      collagen III signal sequence.

<400> 13
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caattgagtt tcactgattt gggcttacca cctactgacc acctccaggc ctcatttgga   180

tttcagacct ttcaacccag tggcatatta ttagatcatc agacatggac aaggaacctg   240

caggtcactc tggaagatgg ttacattgaa ttgagcacca gcgatagcgg cggcccaatt   300

tttaaatctc cacagacgta tatggatggt ttactgcatt atgtatctgt aataagcgac   360

aactctggac tacggcttct catcgatgac cagcttctga gaaatagcaa aaggctaaaa   420

cacatttcaa gttcccggca gtctctgcgt ctgggcggga gcaattttga gggttgtatt   480

agcaatgttt ttgtccagag gttatcactg agtcctgaag tcctagattt gaccagtaac   540

tctctcaaga gagatgtgtc cctgggaggc tgcagtttaa acaaaccacc ttttctaatg   600

ttgcttaaag gttctaccag gtttaacaag accaagactt ttcgtatcaa ccagctgttg   660

caggacacac cagtggcctc cccaaggagc gtgaaggtgt ggcaagatgc taatggtcaa   720

ggacctcaag gccccaaggg agatccaggc cctcctggta ttcctgggag aaatggtgac   780

cctggtattc caggacaacc agggtcccct ggttctcctg gcccccctgg aatctgtgaa   840

tcatgcccta ctggtcctca gaactattct ccccagtatg attcatatga tgtcaagtct   900

ggagtagcag taggaggact cgcaggctat cctggaccag ctggcccccc aggccctccc   960

ggtccccctg gtacatctgg tcatcctggt tcccctggat ctccaggata ccaaggaccc   1020

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cctggtgaac ctgggcaagc tggtccttca ggccctccag gacctcctgg tgctataggt    1080

ccatctggtc ctgctggaaa agatggagaa tcaggtagac ccggacgacc tggagagcga    1140

ggattgcctg gacctccagg tatcaaaggt ccagctggga tacctggatt ccctggtatg    1200

aaaggacaca gaggcttcga tggacgaaat ggagaaaagg gtgaaacagg tgctcctgga    1260

ttaaagggtg aaaatggtct tccaggcgaa aatggagctc ctggacccat gggtccaaga    1320

ggggctcctg gtgagcgagg acggccagga cttcctgggg ctgcaggtgc tcggggtaat    1380

gacggtgctc gaggcagtga tggtcaacca ggccctcctg gtcctcctgg aactgccgga    1440

ttccctggat cccctggtgc taagggtgaa gttggacctg cagggtctcc tggttcaaat    1500

ggtgcccctg gacaaagagg agaacctgga cctcagggac acgctggtgc tcaaggtcct    1560

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cccggaccac gtggtgaacg cggtgaggct ggtattccag gtgttccagg agctaaaggc    1800

gaagatggca aggatggatc acctggagaa cctggtgcaa atgggcttcc aggagctgca    1860

ggagaaaggg gtgcccctgg gttccgagga cctgctggac caaatggcat cccaggagaa    1920

aagggtcctg ctggagagcg tggtgctcca ggccctgcag ggcccagagg agctgctgga    1980

gaacctggca gagatggcgt ccctggaggt ccaggaatga ggggcatgcc cggaagtcca    2040

ggaggaccag gaagtgatgg gaaaccaggg cctcccggaa gtcaaggaga aagtggtcga    2100

ccaggtcctc ctgggccatc tggtccccga ggtcagcctg gtgtcatggg cttccccggt    2160

cctaaaggaa atgatggtgc tcctggtaag aatggagaac gaggtggccc tggaggacct    2220

ggccctcagg gtcctcctgg aaagaatggt gaaactggac ctcaaggacc cccagggcct    2280

actgggcctg gtggtgacaa aggagacaca ggacccccctg gtccacaagg attacaaggc    2340

ttgcctggta caggtggtcc tccaggagaa aatggaaaac tggggaacc aggtccaaag    2400

ggtgatgccg gtgcacctgg agctccagga ggcaagggtg atgctggtgc ccctggtgaa    2460

cgtggacctc ctggattggc aggggcccca ggacttagag gtggagctgg tcccccctggt    2520

cccgaaggag gaaagggtgc tgctggtcct cctgggccac ctggtgctgc tggtactcct    2580

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aagggtgaac caggcggccc aggtgctgat ggtgtcccag ggaaagatgg cccaaggggt    2700

cctactggtc ctattggtcc tcctggccca gctggccagc ctggagataa gggtgaaggt    2760
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cgtggcagtc ctggtggacc tggtgctgct ggcttccctg gtgctcgtgg tcttcctggt   3060

cctcctggta gtaatggtaa cccaggaccc ccaggtccca gcggttctcc aggcaaggat   3120

gggcccccag gtcctgcggg taacactggt gctcctggca gccctggagt gtctggacca   3180

aaaggtgatg ctggccaacc aggagagaag ggatcgcctg gtgcccaggg cccaccagga   3240

gctccaggcc cacttgggat tgctgggatc actggagcac ggggtcttgc aggaccacca   3300

ggcatgccag gtcctagggg aagccctggc cctcagggtg tcaagggtga aagtgggaaa   3360

ccaggagcta acggtctcag tggagaacgt ggtccccctg accccagggt cttcctggt    3420

ctggctggta cagctggtga acctggaaga gatggaaacc ctggatcaga tggtcttcca   3480

ggccgagatg gatctcctgg tggcaagggt gatcgtggtg aaaatggctc tcctggtgcc   3540

cctggcgctc ctggtcatcc aggcccacct ggtcctgtcg gtccagctgg aaagagtggt   3600

gacagaggag aaagtggccc tgctggccct gctggtgctc ccggtcctgc tggttcccga   3660

ggtgctcctg gtcctcaagg cccacgtggt gacaaaggtg aaacaggtga acgtggagct   3720

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ccagggcctc gaggtaacag aggtgaaaga ggatctgagg gctcccagg ccacccaggg    3960

caaccaggcc ctcctggacc tcctggtgcc cctggtcctt gctgtggtgg tgttggagcc   4020

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gaaccaatgg atttcaaaat caacaccgat gagattatga cttcactcaa gtctgttaat   4140

ggacaaatag aaagcctcat tagtcctgat ggttctcgta aaaacccgc tagaaactgc     4200

agagacctga aattctgcca tcctgaactc aagagtggag aatactgggt tgaccctaac   4260

caaggatgca aattggatgc tatcaaggta ttctgtaata tggaaactgg ggaaacatgc   4320

ataagtgcca atcctttgaa tgttccacgg aaacactggt ggacagattc tagtgctgag   4380

aagaaacacg tttggtttgg agagtccatg gatggtggtt ttcagtttag ctacggcaat   4440
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- 18 -

cctgaacttc ctgaagatgt ccttgatgtg cagctggcat tccttcgact tctctccagc   4500

cgagcttccc agaacatcac atatcactgc aaaaatagca ttgcatacat ggatcaggcc   4560

agtggaaatg taaagaaggc cctgaagctg atggggtcaa atgaaggtga attcaaggct   4620

gaaggaaata gcaaattcac ctacacagtt ctggaggatg gttgcacgaa acacactggg   4680

gaatggagca aacagtctt tgaatatcga acacgcaagg ctgtgagact acctattgta   4740

gatattgcac cctatgacat tggtggtcct gatcaagaat ttggtgtgga cgttggccct   4800

gtttgctttt tataa   4815

<210> 14
<211> 1604
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence of modified pro-alpha chain.

<400> 14

Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu
1   5   10   15

His Pro Thr Ile Ile Leu Ala Cys Ser Glu Asp Trp Lys Leu Val Arg
                20   25   30

Ser Ala Ser Phe Ser Arg Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly
            35   40   45

Leu Pro Pro Thr Asp His Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe
        50   55   60

Gln Pro Ser Gly Ile Leu Leu Asp His Gln Thr Trp Thr Arg Asn Leu
65   70   75   80

Gln Val Thr Leu Glu Asp Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser
                85   90   95

Gly Gly Pro Ile Phe Lys Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu
                100   105   110

His Tyr Val Ser Val Ile Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile
        115   120   125

- 19 -

```
Asp Asp Gln Leu Leu Arg Asn Ser Lys Arg Leu Lys His Ile Ser Ser
    130             135             140

Ser Arg Gln Ser Leu Arg Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile
145             150             155             160

Ser Asn Val Phe Val Gln Arg Leu Ser Leu Ser Pro Glu Val Leu Asp
            165             170             175

Leu Thr Ser Asn Ser Leu Lys Arg Asp Val Ser Leu Gly Gly Cys Ser
            180             185             190

Leu Asn Lys Pro Pro Phe Leu Met Leu Leu Lys Gly Ser Thr Arg Phe
            195             200             205

Asn Lys Thr Lys Thr Phe Arg Ile Asn Gln Leu Leu Gln Asp Thr Pro
    210             215             220

Val Ala Ser Pro Arg Ser Val Lys Val Trp Gln Asp Ala Asn Gly Gln
225             230             235             240

Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly
            245             250             255

Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln Pro Gly Ser Pro Gly Ser
            260             265             270

Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn
            275             280             285

Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val Lys Ser Gly Val Ala Val
    290             295             300

Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala Gly Pro Pro Gly Pro Pro
305             310             315             320

Gly Pro Pro Gly Thr Ser Gly His Pro Gly Ser Pro Gly Ser Pro Gly
            325             330             335

Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro
            340             345             350

Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser Gly Pro Ala Gly Lys Asp
```

Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly Glu Arg Gly Leu Pro Gly
    370   375   380

Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile Pro Gly Phe Pro Gly Met
385   390   395   400

Lys Gly His Arg Gly Phe Asp Gly Arg Asn Gly Glu Lys Gly Glu Thr
                405   410   415

Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly Leu Pro Gly Glu Asn Gly
                420   425   430

Ala Pro Gly Pro Met Gly Pro Arg Gly Ala Pro Gly Glu Arg Gly Arg
                435   440   445

Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Ala Arg
    450   455   460

Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly Pro Pro Gly Thr Ala Gly
465   470   475   480

Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu Val Gly Pro Ala Gly Ser
                485   490   495

Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg Gly Glu Pro Gly Pro Gln
                500   505   510

Gly His Ala Gly Ala Gln Gly Pro Pro Gly Pro Pro Gly Ile Asn Gly
            515   520   525

Ser Pro Gly Gly Lys Gly Glu Met Gly Pro Ala Gly Ile Pro Gly Ala
    530   535   540

Pro Gly Leu Met Gly Ala Arg Gly Pro Pro Gly Pro Ala Gly Ala Asn
545   550   555   560

Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Glu Pro Gly Lys Asn Gly
                565   570   575

Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu Arg Gly Glu Ala Gly Ile
            580   585   590

Pro Gly Val Pro Gly Ala Lys Gly Glu Asp Gly Lys Asp Gly Ser Pro
        595   600   605

Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly Ala Ala Gly Glu Arg Gly
        610   615   620

Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro Asn Gly Ile Pro Gly Glu
625   630   635   640

Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro Gly Pro Ala Gly Pro Arg
                645   650   655

Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly Val Pro Gly Gly Pro Gly
                660   665   670

Met Arg Gly Met Pro Gly Ser Pro Gly Gly Pro Gly Ser Asp Gly Lys
            675   680   685

Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser Gly Arg Pro Gly Pro Pro
        690   695   700

Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly
705   710   715   720

Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys Asn Gly Glu Arg Gly Gly
                725   730   735

Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro Gly Lys Asn Gly Glu Thr
            740   745   750

Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly Pro Gly Gly Asp Lys Gly
        755   760   765

Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu Gln Gly Leu Pro Gly Thr
770   775   780

Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro Gly Glu Pro Gly Pro Lys
785   790   795   800

Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Gly Lys Gly Asp Ala Gly
                805   810   815

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Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu Ala Gly Ala Pro Gly Leu
        820   825   830

Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu Gly Gly Lys Gly Ala Ala
        835   840   845

Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly Thr Pro Gly Leu Gln Gly
    850   855   860

Met Pro Gly Glu Arg Gly Gly Leu Gly Ser Pro Gly Pro Lys Gly Asp
865   870   875   880

Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp Gly Val Pro Gly Lys Asp
                885   890   895

Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly
        900   905   910

Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala Pro Gly Leu Pro Gly Ile
    915   920   925

Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro
    930   935   940

Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly Gln Asn Gly Glu Pro Gly
945   950   955   960

Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu Lys Gly Glu Gly Gly Pro
                965   970   975

Pro Gly Val Ala Gly Pro Pro Gly Gly Ser Gly Pro Ala Gly Pro Pro
        980   985   990

Gly Pro Gln Gly Val Lys Gly Glu Arg Gly Ser Pro Gly Gly Pro Gly
        995   1000   1005

Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu Pro Gly Pro Pro Gly
    1010   1015   1020

Ser Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser Gly Ser Pro Gly
    1025   1030   1035

Lys Asp Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly Ala Pro Gly
    1040   1045   1050

Ser Pro Gly Val Ser Gly Pro Lys Gly Asp Ala Gly Gln Pro Gly
    1055   1060   1065

Glu Lys Gly Ser Pro Gly Ala Gln Gly Pro Pro Gly Ala Pro Gly
    1070   1075   1080

Pro Leu Gly Ile Ala Gly Ile Thr Gly Ala Arg Gly Leu Ala Gly
    1085   1090   1095

Pro Pro Gly Met Pro Gly Pro Arg Gly Ser Pro Gly Pro Gln Gly
    1100   1105   1110

Val Lys Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly
    1115   1120   1125

Glu Arg Gly Pro Pro Gly Pro Gln Gly Leu Pro Gly Leu Ala Gly
    1130   1135   1140

Thr Ala Gly Glu Pro Gly Arg Asp Gly Asn Pro Gly Ser Asp Gly
    1145   1150   1155

Leu Pro Gly Arg Asp Gly Ser Pro Gly Gly Lys Gly Asp Arg Gly
    1160   1165   1170

Glu Asn Gly Ser Pro Gly Ala Pro Gly Ala Pro Gly His Pro Gly
    1175   1180   1185

Pro Pro Gly Pro Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly
    1190   1195   1200

Glu Ser Gly Pro Ala Gly Pro Ala Gly Ala Pro Gly Pro Ala Gly
    1205   1210   1215

Ser Arg Gly Ala Pro Gly Pro Gln Gly Pro Arg Gly Asp Lys Gly
    1220   1225   1230

Glu Thr Gly Glu Arg Gly Ala Ala Gly Ile Lys Gly His Arg Gly
    1235   1240   1245

Phe Pro Gly Asn Pro Gly Ala Pro Gly Ser Pro Gly Pro Ala Gly

Gln Gln Gly Ala Ile Gly Ser Pro Gly Pro Ala Gly Pro Arg Gly
     1265   1270   1275

Pro Val Gly Pro Ser Gly Pro Pro Gly Lys Asp Gly Thr Ser Gly
     1280   1285   1290

His Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly Asn Arg Gly
     1295   1300   1305

Glu Arg Gly Ser Glu Gly Ser Pro Gly His Pro Gly Gln Pro Gly
     1310   1315   1320

Pro Pro Gly Pro Pro Gly Ala Pro Gly Pro Cys Cys Gly Gly Val
     1325   1330   1335

Gly Ala Ala Ala Ile Ala Gly Ile Gly Gly Glu Lys Ala Gly Gly
     1340   1345   1350

Phe Ala Pro Tyr Tyr Gly Asp Glu Pro Met Asp Phe Lys Ile Asn
     1355   1360   1365

Thr Asp Glu Ile Met Thr Ser Leu Lys Ser Val Asn Gly Gln Ile
     1370   1375   1380

Glu Ser Leu Ile Ser Pro Asp Gly Ser Arg Lys Asn Pro Ala Arg
     1385   1390   1395

Asn Cys Arg Asp Leu Lys Phe Cys His Pro Glu Leu Lys Ser Gly
     1400   1405   1410

Glu Tyr Trp Val Asp Pro Asn Gln Gly Cys Lys Leu Asp Ala Ile
     1415   1420   1425

Lys Val Phe Cys Asn Met Glu Thr Gly Glu Thr Cys Ile Ser Ala
     1430   1435   1440

Asn Pro Leu Asn Val Pro Arg Lys His Trp Trp Thr Asp Ser Ser
     1445   1450   1455

Ala Glu Lys Lys His Val Trp Phe Gly Glu Ser Met Asp Gly Gly
     1460   1465   1470

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Phe Gln  Phe Ser Tyr Gly Asn  Pro Glu Leu Pro Glu  Asp Val Leu
    1475                 1480              1485


Asp Val  Gln Leu Ala Phe Leu  Arg Leu Leu Ser Ser  Arg Ala Ser
    1490                 1495              1500


Gln Asn  Ile Thr Tyr His Cys  Lys Asn Ser Ile Ala  Tyr Met Asp
    1505                 1510              1515


Gln Ala  Ser Gly Asn Val Lys  Lys Ala Leu Lys Leu  Met Gly Ser
    1520                 1525              1530


Asn Glu  Gly Glu Phe Lys Ala  Glu Gly Asn Ser Lys  Phe Thr Tyr
    1535                 1540              1545


Thr Val  Leu Glu Asp Gly Cys  Thr Lys His Thr Gly  Glu Trp Ser
    1550                 1555              1560


Lys Thr  Val Phe Glu Tyr Arg  Thr Arg Lys Ala Val  Arg Leu Pro
    1565                 1570              1575


Ile Val  Asp Ile Ala Pro Tyr  Asp Ile Gly Gly Pro  Asp Gln Glu
    1580                 1585              1590


Phe Gly  Val Asp Val Gly Pro  Val Cys Phe Leu
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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  PCR primer

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<212>  DNA
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<220>
<223>  PCR primer
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<220>
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<220>
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<210>  19
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<220>
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gtaatacgac tcactatagg gc                                            22


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agggaatccg gcagttcc                                             18


<210>  25
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<210>  26
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<211> 4719
<212> DNA
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<220>
<223> DNA molecule based on procollagen type III N-propeptide.
     Procollagen type III N-propeptide sequence replaced with the
     sequence for SLPI whilst retaining the collagen III signal
     sequence.

<400> 26

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gcccagtgcc ttagatacaa gaaacctgag tgccagagtg actggcagtg tccagggaag       180

aagagatgtt gtcctgacac ttgtggcatc aaatgcctgg atcctgttga caccccaaac       240

ccaacaagga ggaagcctgg gaagtgccca gtgacttatg ccaatgtttt gatgcttaac       300

cccccaatt tctgtgagat ggatggccag tgcaagcgtg acttgaagtg ttgcatgggc        360

atgtgtggga atcctgcgt ttcccctgtg aaagctgctg ttgaaggagg atgttcccat        420

cttggtcagt cctatgcgga tagagatgtc tggaagccag aaccatgcca aatatgtgtc       480

tgtgactcag gatccgttct ctgcgatgac ataatatgtg acgatcaaga attagactgc       540

cccaacccag aaattccatt ggagaatgt tgtgcagttt gcccacagcc tccaactgct        600

cctactcgcc ctcctaatgg tcaaggacct caaggcccca agggagatcc aggccctcct       660

ggtattcctg ggagaaatgg tgaccctggt attccaggac aaccagggtc ccctggttct       720

cctggcccc ctggaatctg tgaatcatgc cctactggtc ctcagaacta ttctcccccag       780

tatgattcat atgatgtcaa gtctggagta gcagtaggag gactcgcagg ctatcctgga       840

ccagctggcc ccccaggccc tcccggtccc cctggtacat ctggtcatcc tggttcccct       900

ggatctccag gataccaagg acccctggt gaacctgggc aagctggtcc ttcaggccct        960

ccaggacctc ctggtgctat aggtccatct ggtcctgctg gaaaagatgg agaatcaggt      1020

agacccggac gacctggaga gcgaggattg cctggacctc caggtatcaa aggtccagct      1080

gggataccctg gattccctgg tatgaaagga cacagaggct cgatggacg aaatggagaa      1140

aagggtgaaa caggtgctcc tggattaaag ggtgaaaatg gtcttccagg cgaaaatgga      1200

gctcctggac ccatgggtcc aagaggggct cctggtgagc gaggacggcc aggacttcct      1260

ggggctgcag gtgctcgggg taatgacggt gctcgaggca gtgatggtca accaggccct      1320

cctggtcctc ctggaactgc cggattccct ggatcccctg gtgctaaggg tgaagttgga      1380
```

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```
cctgcagggt ctcctggttc aaatggtgcc cctggacaaa gaggagaacc tggacctcag    1440

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aaaggcgaaa tgggtcccgc tggcattcct ggagctcctg gactgatggg agcccggggt    1560

cctccaggac cagccggtgc taatggtgct cctggactgc gaggtggtgc aggtgagcct    1620

ggtaagaatg gtgccaaagg agagcccgga ccacgtggtg aacgcggtga ggctggtatt    1680

ccaggtgttc caggagctaa aggcgaagat ggcaaggatg gatcacctgg agaacctggt    1740

gcaaatgggc ttccaggagc tgcaggagaa aggggtgccc ctgggttccg aggacctgct    1800

ggaccaaatg gcatcccagg agaaaagggt cctgctggag agcgtggtgc tccaggccct    1860

gcagggccca gaggagctgc tggagaacct ggcagagatg gcgtccctgg aggtccagga    1920

atgaggggca tgcccggaag tccaggagga ccaggaagtg atgggaaacc agggcctccc    1980

ggaagtcaag gagaaagtgg tcgaccaggt cctcctgggc catctggtcc ccgaggtcag    2040

cctggtgtca tgggcttccc cggtcctaaa ggaaatgatg gtgctcctgg taagaatgga    2100

gaacgaggtg ccctggagg acctggccct cagggtcctc ctggaaagaa tggtgaaact    2160

ggacctcaag gaccccagg gcctactggg cctggtggtg acaaaggaga cacaggaccc    2220

cctggtccac aaggattaca aggcttgcct ggtacaggtg gtcctccagg agaaaatgga    2280

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cccagcggtt ctccaggcaa ggatgggccc ccaggtcctg cgggtaacac tggtgctcct    3060

ggcagccctg gagtgtctgg accaaaaggt gatgctggcc aaccaggaga gaagggatcg    3120
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cctggtgccc aggggcccacc aggagctcca ggcccacttg ggattgctgg gatcactgga      3180

gcacggggtc ttgcaggacc accaggcatg ccaggtccta ggggaagccc tggccctcag      3240

ggtgtcaagg gtgaaagtgg gaaaccagga gctaacggtc tcagtggaga acgtggtccc      3300

cctggacccc agggtcttcc tggtctggct ggtacagctg gtgaacctgg aagagatgga      3360

aaccctggat cagatggtct tccaggccga gatggatctc ctggtggcaa gggtgatcgt      3420

ggtgaaaatg gctctcctgg tgccctggc gctcctggtc atccaggccc acctggtcct      3480

gtcggtccag ctggaaagag tggtgacaga ggagaaagtg gccctgctgg ccctgctggt      3540

gctcccggtc ctgctggttc ccgaggtgct cctggtcctc aaggcccacg tggtgacaaa      3600

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cctgcaggcc ccagaggacc tgttggaccc agtggacctc ctggcaaaga tggaaccagt      3780

ggacatccag gtcccattgg accaccaggg cctcgaggta acagaggtga aagaggatct      3840

gagggctccc caggccaccc agggcaacca ggccctcctg gacctcctgg tgcccctggt      3900

ccttgctgtg gtggtgttgg agccgctgcc attgctggga ttggaggtga aaaagctggc      3960

ggttttgccc cgtattatgg agatgaacca atggatttca aaatcaacac cgatgagatt      4020

atgacttcac tcaagtctgt taatggacaa atagaaagcc tcattagtcc tgatggttct      4080

cgtaaaaacc ccgctagaaa ctgcagagac ctgaaattct gccatcctga actcaagagt      4140

ggagaatact gggttgaccc taaccaagga tgcaaattgg atgctatcaa ggtattctgt      4200

aatatggaaa ctgggggaaac atgcataagt gccaatcctt tgaatgttcc acggaaacac      4260

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ggttttcagt ttagctacgg caatcctgaa cttcctgaag atgtccttga tgtgcagctg      4380

gcattccttc gacttctctc cagccgagct tcccagaaca tcacatatca ctgcaaaaat      4440

agcattgcat acatggatca ggccagtgga aatgtaaaga aggccctgaa gctgatgggg      4500

tcaaatgaag gtgaattcaa ggctgaagga aatagcaaat tcacctacac agttctggag      4560

gatggttgca cgaaacacac tgggggaatgg agcaaaacag tctttgaata tcgaacacgc      4620

aaggctgtga gactacctat tgtagatatt gcaccctatg acattggtgg tcctgatcaa      4680

gaatttggtg tggacgttgg ccctgtttgc ttttttataa                           4719
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<210> 27

<211> 1572
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence of modified pro-alpha chain.

<400> 27

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Met Lys Ser Ser Gly Leu Phe Pro Phe Leu Val Leu Leu Ala Leu Gly
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Thr Leu Ala Pro Trp Ala Val Glu Gly Ser Gly Lys Ser Phe Lys Ala
            20                  25                  30


Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys
            35                  40                  45


Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys
    50                  55                  60


Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn
65                  70                  75                  80


Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys
                85                  90                  95


Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys
                100                 105                 110


Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser
            115                 120                 125


Pro Val Lys Ala Ala Val Glu Gly Gly Cys Ser His Leu Gly Gln Ser
    130                 135                 140


Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Gln Ile Cys Val
145                 150                 155                 160


Cys Asp Ser Gly Ser Val Leu Cys Asp Asp Ile Ile Cys Asp Asp Gln
                165                 170                 175


Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro Phe Gly Glu Cys Cys Ala
                180                 185                 190
```

```
Val Cys Pro Gln Pro Pro Thr Ala Pro Thr Arg Pro Pro Asn Gly Gln
        195                 200             205

Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly
    210             215             220

Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln Pro Gly Ser Pro Gly Ser
225             230             235             240

Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn
            245             250             255

Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val Lys Ser Gly Val Ala Val
        260             265             270

Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala Gly Pro Pro Gly Pro Pro
        275             280             285

Gly Pro Pro Gly Thr Ser Gly His Pro Gly Ser Pro Gly Ser Pro Gly
    290             295             300

Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln Ala Gly Pro Ser Gly Pro
305             310             315             320

Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser Gly Pro Ala Gly Lys Asp
            325             330             335

Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly Glu Arg Gly Leu Pro Gly
        340             345             350

Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile Pro Gly Phe Pro Gly Met
        355             360             365

Lys Gly His Arg Gly Phe Asp Gly Arg Asn Gly Glu Lys Gly Glu Thr
    370             375             380

Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly Leu Pro Gly Glu Asn Gly
385             390             395             400

Ala Pro Gly Pro Met Gly Pro Arg Gly Ala Pro Gly Glu Arg Gly Arg
            405             410             415

Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Ala Arg
```

Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly Pro Pro Gly Thr Ala Gly
        435   440   445

Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu Val Gly Pro Ala Gly Ser
    450   455   460

Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg Gly Glu Pro Gly Pro Gln
465   470   475   480

Gly His Ala Gly Ala Gln Gly Pro Pro Gly Pro Pro Gly Ile Asn Gly
                485   490   495

Ser Pro Gly Gly Lys Gly Glu Met Gly Pro Ala Gly Ile Pro Gly Ala
        500   505   510

Pro Gly Leu Met Gly Ala Arg Gly Pro Pro Gly Pro Ala Gly Ala Asn
        515   520   525

Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Glu Pro Gly Lys Asn Gly
    530   535   540

Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu Arg Gly Glu Ala Gly Ile
545   550   555   560

Pro Gly Val Pro Gly Ala Lys Gly Glu Asp Gly Lys Asp Gly Ser Pro
                565   570   575

Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly Ala Ala Gly Glu Arg Gly
        580   585   590

Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro Asn Gly Ile Pro Gly Glu
        595   600   605

Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro Gly Pro Ala Gly Pro Arg
    610   615   620

Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly Val Pro Gly Gly Pro Gly
625   630   635   640

Met Arg Gly Met Pro Gly Ser Pro Gly Gly Pro Gly Ser Asp Gly Lys
                645   650   655

```
Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser Gly Arg Pro Gly Pro Pro
        660                 665                 670

Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly
        675                 680                 685

Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys Asn Gly Glu Arg Gly Gly
    690                 695                 700

Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro Gly Lys Asn Gly Glu Thr
705                 710                 715                 720

Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly Pro Gly Gly Asp Lys Gly
                725                 730                 735

Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu Gln Gly Leu Pro Gly Thr
            740                 745                 750

Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro Gly Glu Pro Gly Pro Lys
        755                 760                 765

Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Gly Lys Gly Asp Ala Gly
    770                 775                 780

Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu Ala Gly Ala Pro Gly Leu
785                 790                 795                 800

Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu Gly Gly Lys Gly Ala Ala
            805                 810                 815

Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly Thr Pro Gly Leu Gln Gly
        820                 825                 830

Met Pro Gly Glu Arg Gly Gly Leu Gly Ser Pro Gly Pro Lys Gly Asp
        835                 840                 845

Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp Gly Val Pro Gly Lys Asp
    850                 855                 860

Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly
865                 870                 875                 880
```

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```
Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala Pro Gly Leu Pro Gly Ile
            885                 890                 895

Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro
            900                 905                 910

Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly Gln Asn Gly Glu Pro Gly
            915                 920                 925

Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu Lys Gly Glu Gly Gly Pro
    930                 935                 940

Pro Gly Val Ala Gly Pro Pro Gly Gly Ser Gly Pro Ala Gly Pro Pro
945                 950                 955                 960

Gly Pro Gln Gly Val Lys Gly Glu Arg Gly Ser Pro Gly Gly Pro Gly
                965                 970                 975

Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu Pro Gly Pro Pro Gly Ser
            980                 985                 990

Asn Gly Asn Pro Gly Pro Pro Gly  Pro Ser Gly Ser Pro  Gly Lys Asp
        995                 1000                 1005

Gly Pro  Pro Gly Pro Ala Gly  Asn Thr Gly Ala Pro  Gly Ser Pro
    1010                 1015                 1020

Gly Val  Ser Gly Pro Lys Gly  Asp Ala Gly Gln Pro  Gly Glu Lys
    1025                 1030                 1035

Gly Ser  Pro Gly Ala Gln Gly  Pro Pro Gly Ala Pro  Gly Pro Leu
    1040                 1045                 1050

Gly Ile  Ala Gly Ile Thr Gly  Ala Arg Gly Leu Ala  Gly Pro Pro
    1055                 1060                 1065

Gly Met  Pro Gly Pro Arg Gly  Ser Pro Gly Pro Gln  Gly Val Lys
    1070                 1075                 1080

Gly Glu  Ser Gly Lys Pro Gly  Ala Asn Gly Leu Ser  Gly Glu Arg
    1085                 1090                 1095
```

```
Gly Pro  Pro Gly Pro Gln Gly  Leu Pro Gly Leu Ala  Gly Thr Ala
    1100             1105             1110

Gly Glu  Pro Gly Arg Asp Gly  Asn Pro Gly Ser Asp  Gly Leu Pro
    1115             1120             1125

Gly Arg  Asp Gly Ser Pro Gly  Gly Lys Gly Asp Arg  Gly Glu Asn
    1130             1135             1140

Gly Ser  Pro Gly Ala Pro Gly  Ala Pro Gly His Pro  Gly Pro Pro
    1145             1150             1155

Gly Pro  Val Gly Pro Ala Gly  Lys Ser Gly Asp Arg  Gly Glu Ser
    1160             1165             1170

Gly Pro  Ala Gly Pro Ala Gly  Ala Pro Gly Pro Ala  Gly Ser Arg
    1175             1180             1185

Gly Ala  Pro Gly Pro Gln Gly  Pro Arg Gly Asp Lys  Gly Glu Thr
    1190             1195             1200

Gly Glu  Arg Gly Ala Ala Gly  Ile Lys Gly His Arg  Gly Phe Pro
    1205             1210             1215

Gly Asn  Pro Gly Ala Pro Gly  Ser Pro Gly Pro Ala  Gly Gln Gln
    1220             1225             1230

Gly Ala  Ile Gly Ser Pro Gly  Pro Ala Gly Pro Arg  Gly Pro Val
    1235             1240             1245

Gly Pro  Ser Gly Pro Pro Gly  Lys Asp Gly Thr Ser  Gly His Pro
    1250             1255             1260

Gly Pro  Ile Gly Pro Pro Gly  Pro Arg Gly Asn Arg  Gly Glu Arg
    1265             1270             1275

Gly Ser  Glu Gly Ser Pro Gly  His Pro Gly Gln Pro  Gly Pro Pro
    1280             1285             1290

Gly Pro  Pro Gly Ala Pro Gly  Pro Cys Cys Gly Gly  Val Gly Ala
    1295             1300             1305

Ala Ala  Ile Ala Gly Ile Gly  Gly Glu Lys Ala Gly  Gly Phe Ala
```

Pro Tyr Tyr Gly Asp Glu Pro Met Asp Phe Lys Ile Asn Thr Asp
    1325   1330   1335

Glu Ile Met Thr Ser Leu Lys Ser Val Asn Gly Gln Ile Glu Ser
    1340   1345   1350

Leu Ile Ser Pro Asp Gly Ser Arg Lys Asn Pro Ala Arg Asn Cys
    1355   1360   1365

Arg Asp Leu Lys Phe Cys His Pro Glu Leu Lys Ser Gly Glu Tyr
    1370   1375   1380

Trp Val Asp Pro Asn Gln Gly Cys Lys Leu Asp Ala Ile Lys Val
    1385   1390   1395

Phe Cys Asn Met Glu Thr Gly Glu Thr Cys Ile Ser Ala Asn Pro
    1400   1405   1410

Leu Asn Val Pro Arg Lys His Trp Trp Thr Asp Ser Ser Ala Glu
    1415   1420   1425

Lys Lys His Val Trp Phe Gly Glu Ser Met Asp Gly Gly Phe Gln
    1430   1435   1440

Phe Ser Tyr Gly Asn Pro Glu Leu Pro Glu Asp Val Leu Asp Val
    1445   1450   1455

Gln Leu Ala Phe Leu Arg Leu Leu Ser Ser Arg Ala Ser Gln Asn
    1460   1465   1470

Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp Gln Ala
    1475   1480   1485

Ser Gly Asn Val Lys Lys Ala Leu Lys Leu Met Gly Ser Asn Glu
    1490   1495   1500

Gly Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe Thr Tyr Thr Val
    1505   1510   1515

Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp Ser Lys Thr
    1520   1525   1530

```
Val Phe  Glu Tyr Arg Thr Arg  Lys Ala Val Arg Leu  Pro Ile Val
    1535             1540             1545


Asp Ile  Ala Pro Tyr Asp Ile  Gly Gly Pro Asp Gln  Glu Phe Gly
    1550             1555             1560


Val Asp  Val Gly Pro Val Cys  Phe Leu
    1565             1570
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<210>  28
<211>  11
<212>  PRT
<213>  Unknown


<220>
<223>  Sequence typically found in small leucine-rich proteoglycans.


<220>
<221>  MISC_FEATURE
<222>  (2)..(3)
<223>  X at polition 2 or 3 may be any amino acid.

<220>
<221>  MISC_FEATURE
<222>  (5)..(5)
<223>  X at polition 5 may be any amino acid.

<220>
<221>  MISC_FEATURE
<222>  (7)..(8)
<223>  X at polition 7 or 8 may be any amino acid.

<220>
<221>  MISC_FEATURE
<222>  (10)..(10)
<223>  X at polition 10 may be any amino acid.

<220>
<221>  MISC_FEATURE
<222>  (11)..(11)
<223>  X at polition 11 is selected from L and I only.

<400>  28

Leu Xaa Xaa Leu Xaa Leu Xaa Xaa Asn Xaa Xaa
1               5                   10
```

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